

```

<!--StartFragment-->RESULT 5
BH789726/c
LOCUS      BH789726                      65 bp      DNA      linear      GSS 02-APR-2002
DEFINITION SALK_044532.19.55.x Arabidopsis thaliana TDNA insertion lines
            Arabidopsis thaliana genomic clone SALK_044532.19.55.x, genomic
            survey sequence.
ACCESSION  BH789726
VERSION    BH789726.1  GI:19882824
KEYWORDS    GSS.
SOURCE      Arabidopsis thaliana (thale cress)
  ORGANISM  Arabidopsis thaliana
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
            rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE  1  (bases 1 to 65)
  AUTHORS  Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R.,
            Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L.,
            Shinn,P., Zimmerman,J. and Ecker,J.R.
  TITLE    A Sequence-Indexed Library of Insertion Mutations in the
            Arabidopsis Genome
  JOURNAL   Unpublished (2001)
COMMENT    Contact: Joseph R. Ecker
            Salk Institute Genomic Analysis Laboratory (SIGnAL)
            The Salk Institute for Biological Studies
            10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
            Tel: 858 453 4100 x1752
            Fax: 858 558 6379
            Email: ecker@salk.edu
            This is single pass sequence recovered from the left border of
            TDNA. This sequence lies within an annotated exon of At3g41627.
            Class: TDNA tagged.
FEATURES   Location/Qualifiers
  source    1..65
            /organism="Arabidopsis thaliana"
            /mol_type="genomic DNA"
            /ecotype="Col-0"
            /db_xref="taxon:3702"
            /clone="SALK_044532.19.55.x"
            /clone_lib="Arabidopsis thaliana TDNA insertion lines"
            /note="PCR was performed on Arabidopsis thaliana lines
            each of which contains one or more TDNA insertion
            elements. The resultant fragment for each line was
            directly sequenced to determine the genomic sequence at
            the site of insertion. Details of the protocols used can
            be found at http://signal.salk.edu/tdna\_protocols.html"
ORIGIN

  Query Match      100.0%;  Score 12;  DB 15;  Length 65;
  Best Local Similarity 100.0%;  Pred. No. 3.7e+04;
  Matches 12;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

Qy      1  GCCAGCGGAGTC 12
        |||||
Db      21  GCCAGCGGAGTC 10

<!--EndFragment-->

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